

109672

Schreiber, David

From: Steadman, David (AU1652)
Sent: Thursday, November 13, 2003 9:51 AM
To: Schreiber, David
Subject: 09/508,418 sequence search request

NAME: David Steadman

AU: 1652

Date: 11/13/03

Office: 10D-04

Mailbox: 10D-01

Mr. Schreiber, please search the following sequences in commercial and interference databases:

1) Standard search of SEQ ID NO:2 against amino acid databases.

2) Standard search of SEQ ID NO:2 against nucleic acid databases.

Please save results to diskette.

Thank you very much.

David J. Steadman
Patent Examiner
Art Unit 1652
Crystal Mall 1, Room 10D-04
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RESULT 1

T04058

protoporphyrinogen oxidase (EC 1.3.3.4) IX precursor, chloroplast - common tobacco

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000

C;Accession: T04058

R;Lermontova, I.; Kruse, E.; Mock, H.P.; Grimm, B.

Proc. Natl. Acad. Sci. U.S.A. 94, 8895-8900, 1997

A;Title: Cloning and characterization of a plastidal and a mitochondrial isoform of tobacco protoporphyrinogen IX oxidase.

A;Reference number: Z15186; MUID:97385200; PMID:9238074

A;Accession: T04058

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-548 <LER>

A;Cross-references: EMBL:Y13465; NID:g2370332; PIDN:CAA73865.1; PID:g2370333

A;Experimental source: strain SR1

C;Genetics:

A;Gene: ppxI

C;Function:

A;Pathway: tetrapyrrole synthesis

C;Keywords: chloroplast; oxidoreductase

F;1-50/Domain: transit peptide (chloroplast) #status predicted <TNP>

F;51-548/Product: protoporphyrinogen oxidase IX #status predicted <MAT>

Query Match 99.2%; Score 2821; DB 2; Length 548;
Best Local Similarity 99.3%; Pred. No. 4.3e-200;
Matches 544; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MTTTPIANHPNIFTHQSSSSPLAFLNRTSFIPFSSISKRNSVNCNGWRTRCSVAKDYTVP 60
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Db 1 MTTTPIANHPNIFTHQSSSSPLAFLNRTSFIPFSSISKRNSVNCNGWRTRCSVAKDYTVP 60

Qy 61 SSAVDGGPAAELDCVIVGAGISGLCIAQVMSANYPNLMVTEARDRAGGNITTVERDGYLW 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 SSAVDGGPAAELDCVIVGAGISGLCIAQVMSANYPNLMVTEARDRAGGNITTVERDGYLW 120

Qy 121 EEGPNSFQPSDPMLTMAVDCGLKDDLVLGDPNAPRFVWLKGKLRPVPSKLTDLPPFDLMS 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 EEGPNSFQPSDPMLTMAVDCGLKDDLVLGDPNAPRFVWLKGKLRPVPSKLTDLAFFDLMS 180

Qy 181 IPGKLRAFGPIGLRSPPGHEESEVEQFVRRNLGGEVFERLIEPFCGVYVGDP SKLSMK 240
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Db 181 IPGKLRAFGAIGL RSPPGHEESEVEQFVRRNLGGEVFERLIEPFCGVYAGDPSKLSMK 240

Qy 241 AAFGKVWKLEETGGSIIGGTFKAIKERSSTPKAPRDPRLPKPKGQTVGSFRKGLRMLPDA 300
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Db 241 AAFGKVWKLEETGGSIIGGTFKAIKERSSTPKAPRDPRLPKPKGQTVGSFRKGLRMLPDA 300

Qy 301 ISARLGSKLKLSWKLSSITKSEKGGYHLYTETPEGVVS LQSR SIVMTVPSYVASNILRPL 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 301 ISARLGSKLKLSWKLSSITKSEKGGYHLYTETPEGVVS LQSR SIVMTVPSYVASNILRPL 360

Qy 361 SVAAADALSNFYYPPVGAVTISYPQEAIRDERLVDGELKGFGQLHPRTQGVETLGTIYSS 420
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 361 SVAAADALSNFYYPPVGAVTITYPQEAIRDERLVDGELKGFGQLHPRTQGVETLGTIYSS 420

Qy 421 SLFPNRAPKGRVLLLNYIGGAKNPEILSKTESQLVEVVDRLRKMLIKPKAQDPLVVGVR 480
|||
Db 421 SLFPNRAPKGRVLLLNYIGGAKNPEILSKTESQLVEVVDRLRKMLIKPKAQDPLVVGVR 480

Qy 481 VWPQAIPQFLVGHLDTLSTAKAAMNDNGLEGLFLGGNYVSGVALGRCVEGAYEVASEVTG 540
|||
Db 481 VWPQAIPQFLVGHLDTLSTAKAAMNDNGLEGLFLGGNYVSGVALGRCVEGAYEVASEVTG 540

Qy 541 FLSRYAYK 548
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Db 541 FLSRYAYK 548